

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: POTTER, ANDREW A.  
REDMOND, MARK J.  
HUGHES, HUW P.A.
- (ii) TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
CHIMERAS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: REED & ROBINS
  - (B) STREET: 285 HAMILTON AVENUE, SUITE 200
  - (C) CITY: PALO ALTO
  - (D) STATE: CALIFORNIA
  - (E) COUNTRY: UNITED STATES OF AMERICA
  - (F) ZIP: 94301
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/455,970
  - (B) FILING DATE: 31-MAY-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/960,932
  - (B) FILING DATE: 14-OCT-1992
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: ROBINS, ROBERTA L.
  - (B) REGISTRATION NUMBER: 33,208
  - (C) REFERENCE/DOCKET NUMBER: 9001-0016.10
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 327-3400
  - (B) TELEFAX: (415) 327-3231

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2794 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..2778

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA	48
Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT	96
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG	144
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	
35 40 45	
GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA	192
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA	240
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA	288
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA	336
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA	384
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT	432
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT	480
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT	528
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	
165 170 175	
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA	576
Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys	
180 185 190	
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT	624
Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val	
195 200 205	
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT	672
Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp	
210 215 220	
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA	720
Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala	
225 230 235 240	

AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440

GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GGT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160

GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT TCT CTT CAA TTT GCT AGG GGA TCC Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser 915 920 925	2778
TAGCTAGCTA GCCATG	2794

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 926 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys  
1 5 10 15  
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly  
20 25 30  
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu  
35 40 45  
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu  
50 55 60  
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu  
65 70 75 80  
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln  
85 90 95  
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys  
100 105 110  
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly  
115 120 125  
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu  
130 135 140  
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala  
145 150 155 160  
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe  
165 170 175  
Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys  
180 185 190  
Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val  
195 200 205  
Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp  
210 215 220  
Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala  
225 230 235 240  
Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu  
245 250 255  
Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala  
260 265 270

Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala  
 275 280 285  
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala  
 290 295 300  
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu  
 305 310 315 320  
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn  
 325 330 335  
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly  
 340 345 350  
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly  
 355 360 365  
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His  
 370 375 380  
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn  
 385 390 395 400  
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala  
 405 410 415  
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu  
 420 425 430  
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn  
 435 440 445  
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser  
 450 455 460  
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala  
 465 470 475 480  
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser  
 485 490 495  
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu  
 500 505 510  
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr  
 515 520 525  
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile  
 530 535 540  
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln  
 545 550 555 560  
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys  
 565 570 575  
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe  
 580 585 590  
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg  
 595 600 605

Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr  
 610 615 620  
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr  
 625 630 635 640  
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly  
 645 650 655  
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His  
 660 665 670  
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile  
 675 680 685  
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala  
 690 695 700  
 Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn  
 705 710 715 720  
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn  
 725 730 735  
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly  
 740 745 750  
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp  
 755 760 765  
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser  
 770 775 780  
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile  
 785 790 795 800  
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu  
 805 810 815  
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu  
 820 825 830  
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys  
 835 840 845  
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp  
 850 855 860  
 Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys  
 865 870 875 880  
 Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe  
 885 890 895  
 Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met  
 900 905 910  
 Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser  
 915 920 925



(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCAGCTC TTCTGCCGGC TGCAAAACT TCTTCTGGAA AACCTTCACC AGCTGCTAGG 60

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCTAGC AGCTGGTGAA GGTTTTCCAG AAGAAGTTTT TGCAGCCGGC AGAAGAGCTG 60

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCTCAGCA TTGGAGCTAC GGCCTGCGCC CTGGCTAAG 39

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCTTAGC CAGGGCGCAG GCCGTAGCTC CAATGCTGA 39

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCTTGCAA CATTGTGCCT GTGAGCATTG TGAGCCGCAA CATTGTGTAC ACCCGCGCGC 60  
AACCTAACCA AGACATTGTG TAG 83

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCTACAC AATGTCTTGG TTAAGTTGCG CGCGGGTGTA CACAATGTTG CGGCTCACAA 60  
TCGTACAGG CACAATGTTG CAA 83

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2838 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..2829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA 48  
Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys  
1 5 10 15  
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT 96  
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly  
20 25 30  
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG 144  
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu  
35 40 45

GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu 50 55 60	192
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu 65 70 75 80	240
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln 85 90 95	288
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys 100 105 110	336
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly 115 120 125	384
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu 130 135 140	432
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala 145 150 155 160	480
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe 165 170 175	528
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys 180 185 190	576
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val 195 200 205	624
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp 210 215 220	672
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala 225 230 235 240	720
AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864

GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440
GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584

GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GGT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160
GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304

ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT TCT CTT CAA TTT GCT AGG GGA TCC AGC TCT Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Ser Ser 915 920 925	2784
TCT GCC GGC TGC AAA AAC TTC TTC TGG AAA ACC TTC ACC AGC TGC Ser Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys 930 935 940	2829
TAGGGATCC	2838

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 943 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Thr	Val	Ile	Asp	Leu	Ser	Phe	Pro	Lys	Thr	Gly	Ala	Lys	Lys
1				5					10					15	
Ile	Ile	Leu	Tyr	Ile	Pro	Gln	Asn	Tyr	Gln	Tyr	Asp	Thr	Glu	Gln	Gly
		20					25						30		

Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu  
 35 40 45  
 Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu  
 50 55 60  
 Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu  
 65 70 75 80  
 Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln  
 85 90 95  
 Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys  
 100 105 110  
 Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly  
 115 120 125  
 Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu  
 130 135 140  
 Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala  
 145 150 155 160  
 Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe  
 165 170 175  
 Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys  
 180 185 190  
 Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val  
 195 200 205  
 Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp  
 210 215 220  
 Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala  
 225 230 235 240  
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu  
 245 250 255  
 Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala  
 260 265 270  
 Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala  
 275 280 285  
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala  
 290 295 300  
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu  
 305 310 315 320  
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn  
 325 330 335  
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly  
 340 345 350  
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly  
 355 360 365

Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His  
 370 375 380  
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn  
 385 390 395 400  
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala  
 405 410 415  
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu  
 420 425 430  
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn  
 435 440 445  
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser  
 450 455 460  
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala  
 465 470 475 480  
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser  
 485 490 495  
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu  
 500 505 510  
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr  
 515 520 525  
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile  
 530 535 540  
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln  
 545 550 555 560  
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys  
 565 570 575  
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe  
 580 585 590  
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg  
 595 600 605  
 Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr  
 610 615 620  
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr  
 625 630 635 640  
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly  
 645 650 655  
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His  
 660 665 670  
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile  
 675 680 685  
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala  
 690 695 700



Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn  
 705 710 715 720  
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn  
 725 730 735  
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly  
 740 745 750  
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp  
 755 760 765  
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser  
 770 775 780  
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile  
 785 790 795 800  
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu  
 805 810 815  
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu  
 820 825 830  
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys  
 835 840 845  
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp  
 850 855 860  
 Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys  
 865 870 875 880  
 Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe  
 885 890 895  
 Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met  
 900 905 910  
 Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Ser Ser  
 915 920 925  
 Ser Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys  
 930 935 940

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..2808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA	48
Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT	96
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG	144
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	
35 40 45	
GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA	192
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA	240
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA	288
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA	336
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA	384
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT	432
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT	480
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT	528
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	
165 170 175	
GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA	576
Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys	
180 185 190	
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT	624
Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val	
195 200 205	
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT	672
Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp	
210 215 220	
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA	720
Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala	
225 230 235 240	

AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248
AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440

GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968
AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GGT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160

GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688
ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met 900 905 910	2736
TTG GAT CAA AGT TTA TCT TCT CTT CAA TTT GCT AGG GGA TCT CAG CAT Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Gln His 915 920 925	2784
TGG AGC TAC GGC CTG CGC CCT GGC TAAGGATCC Trp Ser Tyr Gly Leu Arg Pro Gly 930 935	2817

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys  
1 5 10 15  
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly  
20 25 30  
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu  
35 40 45  
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu  
50 55 60  
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu  
65 70 75 80  
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln  
85 90 95  
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys  
100 105 110  
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly  
115 120 125  
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu  
130 135 140  
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala  
145 150 155 160  
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe  
165 170 175  
Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys  
180 185 190  
Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val  
195 200 205  
Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp  
210 215 220  
Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala  
225 230 235 240  
Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu  
245 250 255  
Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala  
260 265 270

Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala  
 275 280 285  
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala  
 290 295 300  
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu  
 305 310 315 320  
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn  
 325 330 335  
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly  
 340 345 350  
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly  
 355 360 365  
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His  
 370 375 380  
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn  
 385 390 395 400  
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala  
 405 410 415  
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu  
 420 425 430  
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn  
 435 440 445  
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser  
 450 455 460  
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala  
 465 470 475 480  
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser  
 485 490 495  
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu  
 500 505 510  
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr  
 515 520 525  
 Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile  
 530 535 540  
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln  
 545 550 555 560  
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys  
 565 570 575  
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe  
 580 585 590  
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg  
 595 600 605

Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr  
610 615 620  
Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr  
625 630 635 640  
Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly  
645 650 655  
Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His  
660 665 670  
Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile  
675 680 685  
Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala  
690 695 700  
Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn  
705 710 715 720  
Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn  
725 730 735  
Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly  
740 745 750  
Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp  
755 760 765  
Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser  
770 775 780  
Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile  
785 790 795 800  
Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu  
805 810 815  
Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu  
820 825 830  
Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys  
835 840 845  
Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp  
850 855 860  
Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys  
865 870 875 880  
Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe  
885 890 895  
Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met  
900 905 910  
Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Gln His  
915 920 925  
Trp Ser Tyr Gly Leu Arg Pro Gly  
930 935



(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2861 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GCT ACT GTT ATA GAT CTA AGC TTC CCA AAA ACT GGG GCA AAA AAA	48
Met Ala Thr Val Ile Asp Leu Ser Phe Pro Lys Thr Gly Ala Lys Lys	
1 5 10 15	
ATT ATC CTC TAT ATT CCC CAA AAT TAC CAA TAT GAT ACT GAA CAA GGT	96
Ile Ile Leu Tyr Ile Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly	
20 25 30	
AAT GGT TTA CAG GAT TTA GTC AAA GCG GCC GAA GAG TTG GGG ATT GAG	144
Asn Gly Leu Gln Asp Leu Val Lys Ala Ala Glu Glu Leu Gly Ile Glu	
35 40 45	
GTA CAA AGA GAA GAA CGC AAT AAT ATT GCA ACA GCT CAA ACC AGT TTA	192
Val Gln Arg Glu Glu Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu	
50 55 60	
GGC ACG ATT CAA ACC GCT ATT GGC TTA ACT GAG CGT GGC ATT GTG TTA	240
Gly Thr Ile Gln Thr Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu	
65 70 75 80	
TCC GCT CCA CAA ATT GAT AAA TTG CTA CAG AAA ACT AAA GCA GGC CAA	288
Ser Ala Pro Gln Ile Asp Lys Leu Leu Gln Lys Thr Lys Ala Gly Gln	
85 90 95	
GCA TTA GGT TCT GCC GAA AGC ATT GTA CAA AAT GCA AAT AAA GCC AAA	336
Ala Leu Gly Ser Ala Glu Ser Ile Val Gln Asn Ala Asn Lys Ala Lys	
100 105 110	
ACT GTA TTA TCT GGC ATT CAA TCT ATT TTA GGC TCA GTA TTG GCT GGA	384
Thr Val Leu Ser Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ala Gly	
115 120 125	
ATG GAT TTA GAT GAG GCC TTA CAG AAT AAC AGC AAC CAA CAT GCT CTT	432
Met Asp Leu Asp Glu Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu	
130 135 140	
GCT AAA GCT GGC TTG GAG CTA ACA AAT TCA TTA ATT GAA AAT ATT GCT	480
Ala Lys Ala Gly Leu Glu Leu Thr Asn Ser Leu Ile Glu Asn Ile Ala	
145 150 155 160	
AAT TCA GTA AAA ACA CTT GAC GAA TTT GGT GAG CAA ATT AGT CAA TTT	528
Asn Ser Val Lys Thr Leu Asp Glu Phe Gly Glu Gln Ile Ser Gln Phe	
165 170 175	

GGT TCA AAA CTA CAA AAT ATC AAA GGC TTA GGG ACT TTA GGA GAC AAA Gly Ser Lys Leu Gln Asn Ile Lys Gly Leu Gly Thr Leu Gly Asp Lys 180 185 190	576
CTC AAA AAT ATC GGT GGA CTT GAT AAA GCT GGC CTT GGT TTA GAT GTT Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val 195 200 205	624
ATC TCA GGG CTA TTA TCG GGC GCA ACA GCT GCA CTT GTA CTT GCA GAT Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp 210 215 220	672
AAA AAT GCT TCA ACA GCT AAA AAA GTG GGT GCG GGT TTT GAA TTG GCA Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala 225 230 235 240	720
AAC CAA GTT GTT GGT AAT ATT ACC AAA GCC GTT TCT TCT TAC ATT TTA Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu 245 250 255	768
GCC CAA CGT GTT GCA GCA GGT TTA TCT TCA ACT GGG CCT GTG GCT GCT Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala 260 265 270	816
TTA ATT GCT TCT ACT GTT TCT CTT GCG ATT AGC CCA TTA GCA TTT GCC Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala 275 280 285	864
GGT ATT GCC GAT AAA TTT AAT CAT GCA AAA AGT TTA GAG AGT TAT GCC Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala 290 295 300	912
GAA CGC TTT AAA AAA TTA GGC TAT GAC GGA GAT AAT TTA TTA GCA GAA Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu 305 310 315 320	960
TAT CAG CGG GGA ACA GGG ACT ATT GAT GCA TCG GTT ACT GCA ATT AAT Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn 325 330 335	1008
ACC GCA TTG GCC GCT ATT GCT GGT GGT GTG TCT GCT GCT GCA GCC GGC Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Gly 340 345 350	1056
TCG GTT ATT GCT TCA CCG ATT GCC TTA TTA GTA TCT GGG ATT ACC GGT Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly 355 360 365	1104
GTA ATT TCT ACG ATT CTG CAA TAT TCT AAA CAA GCA ATG TTT GAG CAC Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His 370 375 380	1152
GTT GCA AAT AAA ATT CAT AAC AAA ATT GTA GAA TGG GAA AAA AAT AAT Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn 385 390 395 400	1200
CAC GGT AAG AAC TAC TTT GAA AAT GGT TAC GAT GCC CGT TAT CTT GCG His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala 405 410 415	1248

AAT TTA CAA GAT AAT ATG AAA TTC TTA CTG AAC TTA AAC AAA GAG TTA Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu 420 425 430	1296
CAG GCA GAA CGT GTC ATC GCT ATT ACT CAG CAG CAA TGG GAT AAC AAC Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn 435 440 445	1344
ATT GGT GAT TTA GCT GGT ATT AGC CGT TTA GGT GAA AAA GTC CTT AGT Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser 450 455 460	1392
GGT AAA GCC TAT GTG GAT GCG TTT GAA GAA GGC AAA CAC ATT AAA GCC Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala 465 470 475 480	1440
GAT AAA TTA GTA CAG TTG GAT TCG GCA AAC GGT ATT ATT GAT GTG AGT Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser 485 490 495	1488
AAT TCG GGT AAA GCG AAA ACT CAG CAT ATC TTA TTC AGA ACG CCA TTA Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu 500 505 510	1536
TTG ACG CCG GGA ACA GAG CAT CGT GAA CGC GTA CAA ACA GGT AAA TAT Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr 515 520 525	1584
GAA TAT ATT ACC AAG CTC AAT ATT AAC CGT GTA GAT AGC TGG AAA ATT Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile 530 535 540	1632
ACA GAT GGT GCA GCA AGT TCT ACC TTT GAT TTA ACT AAC GTT GTT CAG Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln 545 550 555 560	1680
CGT ATT GGT ATT GAA TTA GAC AAT GCT GGA AAT GTA ACT AAA ACC AAA Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys 565 570 575	1728
GAA ACA AAA ATT ATT GCC AAA CTT GGT GAA GGT GAT GAC AAC GTA TTT Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe 580 585 590	1776
GTT GGT TCT GGT ACG ACG GAA ATT GAT GGC GGT GAA GGT TAC GAC CGA Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg 595 600 605	1824
GTT CAC TAT AGC CGT GGA AAC TAT GGT GCT TTA ACT ATT GAT GCA ACC Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr 610 615 620	1872
AAA GAG ACC GAG CAA GGT AGT TAT ACC GTA AAT CGT TTC GTA GAA ACC Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr 625 630 635 640	1920
GGT AAA GCA CTA CAC GAA GTG ACT TCA ACC CAT ACC GCA TTA GTG GGC Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly 645 650 655	1968

AAC CGT GAA GAA AAA ATA GAA TAT CGT CAT AGC AAT AAC CAG CAC CAT Asn Arg Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His 660 665 670	2016
GCC GGT TAT TAC ACC AAA GAT ACC TTG AAA GCT GTT GAA GAA ATT ATC Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile 675 680 685	2064
GGT ACA TCA CAT AAC GAT ATC TTT AAA GGT AGT AAG TTC AAT GAT GCC Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala 690 695 700	2112
TTT AAC GGT GGT GAT GGT GTC GAT ACT ATT GAC GGT AAC GAC GGC AAT Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn 705 710 715 720	2160
GAC CGC TTA TTT GGT GGT AAA GGC GAT GAT ATT CTC GAT GGT GGA AAT Asp Arg Leu Phe Gly Gly Lys Gly Asp Ile Leu Asp Gly Gly Asn 725 730 735	2208
GGT GAT GAT TTT ATC GAT GGC GGT AAA GGC AAC GAC CTA TTA CAC GGT Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly 740 745 750	2256
GGC AAG GGC GAT GAT ATT TTC GTT CAC CGT AAA GGC GAT GGT AAT GAT Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp 755 760 765	2304
ATT ATT ACC GAT TCT GAC GGC AAT GAT AAA TTA TCA TTC TCT GAT TCG Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser 770 775 780	2352
AAC TTA AAA GAT TTA ACA TTT GAA AAA GTT AAA CAT AAT CTT GTC ATC Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile 785 790 795 800	2400
ACG AAT AGC AAA AAA GAG AAA GTG ACC ATT CAA AAC TGG TTC CGA GAG Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu 805 810 815	2448
GCT GAT TTT GCT AAA GAA GTG CCT AAT TAT AAA GCA ACT AAA GAT GAG Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu 820 825 830	2496
AAA ATC GAA GAA ATC ATC GGT CAA AAT GGC GAG CGG ATC ACC TCA AAG Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys 835 840 845	2544
CAA GTT GAT GAT CTT ATC GCA AAA GGT AAC GGC AAA ATT ACC CAA GAT Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp 850 855 860	2592
GAG CTA TCA AAA GTT GTT GAT AAC TAT GAA TTG CTC AAA CAT AGC AAA Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys 865 870 875 880	2640
AAT GTG ACA AAC AGC TTA GAT AAG TTA ATC TCA TCT GTA AGT GCA TTT Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe 885 890 895	2688

ACC TCG TCT AAT GAT TCG AGA AAT GTA TTA GTG GCT CCA ACT TCA ATG	2736
Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met	
900 905 910	
TTG GAT CAA AGT TTA TCT TCT CTT CAA TTT GCT AGG GGA TCT TGC AAC	2784
Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Cys Asn	
915 920 925	
ATT GTG CCT GTG AGC ATT GTG AGC CGC AAC ATT GTG TAC ACC CGC GCG	2832
Ile Val Pro Val Ser Ile Val Ser Arg Asn Ile Val Tyr Thr Arg Ala	
930 935 940	
CAA CCT AAC CAA GAC ATT GTG TAGGATCC	2861
Gln Pro Asn Gln Asp Ile Val	
945 950	

(2) INFORMATION FOR SEQ ID.NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Thr	Val	Ile	Asp	Leu	Ser	Phe	Pro	Lys	Thr	Gly	Ala	Lys	Lys	1	5	10	15
Ile	Ile	Leu	Tyr	Ile	Pro	Gln	Asn	Tyr	Gln	Tyr	Asp	Thr	Glu	Gln	Gly	20	25	30	
Asn	Gly	Leu	Gln	Asp	Leu	Val	Lys	Ala	Ala	Glu	Glu	Leu	Gly	Ile	Glu	35	40	45	
Val	Gln	Arg	Glu	Glu	Arg	Asn	Asn	Ile	Ala	Thr	Ala	Gln	Thr	Ser	Leu	50	55	60	
Gly	Thr	Ile	Gln	Thr	Ala	Ile	Gly	Leu	Thr	Glu	Arg	Gly	Ile	Val	Leu	65	70	75	80
Ser	Ala	Pro	Gln	Ile	Asp	Lys	Leu	Leu	Gln	Lys	Thr	Lys	Ala	Gly	Gln	85	90	95	
Ala	Leu	Gly	Ser	Ala	Glu	Ser	Ile	Val	Gln	Asn	Ala	Asn	Lys	Ala	Lys	100	105	110	
Thr	Val	Leu	Ser	Gly	Ile	Gln	Ser	Ile	Leu	Gly	Ser	Val	Leu	Ala	Gly	115	120	125	
Met	Asp	Leu	Asp	Glu	Ala	Leu	Gln	Asn	Asn	Ser	Asn	Gln	His	Ala	Leu	130	135	140	
Ala	Lys	Ala	Gly	Leu	Glu	Leu	Thr	Asn	Ser	Leu	Ile	Glu	Asn	Ile	Ala	145	150	155	160
Asn	Ser	Val	Lys	Thr	Leu	Asp	Glu	Phe	Gly	Glu	Gln	Ile	Ser	Gln	Phe	165	170	175	
Gly	Ser	Lys	Leu	Gln	Asn	Ile	Lys	Gly	Leu	Gly	Thr	Leu	Gly	Asp	Lys	180	185	190	

Leu Lys Asn Ile Gly Gly Leu Asp Lys Ala Gly Leu Gly Leu Asp Val  
 195 200 205  
 Ile Ser Gly Leu Leu Ser Gly Ala Thr Ala Ala Leu Val Leu Ala Asp  
 210 215 220  
 Lys Asn Ala Ser Thr Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala  
 225 230 235 240  
 Asn Gln Val Val Gly Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu  
 245 250 255  
 Ala Gln Arg Val Ala Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala  
 260 265 270  
 Leu Ile Ala Ser Thr Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala  
 275 280 285  
 Gly Ile Ala Asp Lys Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala  
 290 295 300  
 Glu Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu  
 305 310 315 320  
 Tyr Gln Arg Gly Thr Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn  
 325 330 335  
 Thr Ala Leu Ala Ala Ile Ala Gly Gly Val Ser Ala Ala Ala Ala Gly  
 340 345 350  
 Ser Val Ile Ala Ser Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly  
 355 360 365  
 Val Ile Ser Thr Ile Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His  
 370 375 380  
 Val Ala Asn Lys Ile His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn  
 385 390 395 400  
 His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg Tyr Leu Ala  
 405 410 415  
 Asn Leu Gln Asp Asn Met Lys Phe Leu Leu Asn Leu Asn Lys Glu Leu  
 420 425 430  
 Gln Ala Glu Arg Val Ile Ala Ile Thr Gln Gln Gln Trp Asp Asn Asn  
 435 440 445  
 Ile Gly Asp Leu Ala Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser  
 450 455 460  
 Gly Lys Ala Tyr Val Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala  
 465 470 475 480  
 Asp Lys Leu Val Gln Leu Asp Ser Ala Asn Gly Ile Ile Asp Val Ser  
 485 490 495  
 Asn Ser Gly Lys Ala Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu  
 500 505 510  
 Leu Thr Pro Gly Thr Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr  
 515 520 525

Glu Tyr Ile Thr Lys Leu Asn Ile Asn Arg Val Asp Ser Trp Lys Ile  
 530 535 540  
 Thr Asp Gly Ala Ala Ser Ser Thr Phe Asp Leu Thr Asn Val Val Gln  
 545 550 555 560  
 Arg Ile Gly Ile Glu Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys  
 565 570 575  
 Glu Thr Lys Ile Ile Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe  
 580 585 590  
 Val Gly Ser Gly Thr Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg  
 595 600 605  
 Val His Tyr Ser Arg Gly Asn Tyr Gly Ala Leu Thr Ile Asp Ala Thr  
 610 615 620  
 Lys Glu Thr Glu Gln Gly Ser Tyr Thr Val Asn Arg Phe Val Glu Thr  
 625 630 635 640  
 Gly Lys Ala Leu His Glu Val Thr Ser Thr His Thr Ala Leu Val Gly  
 645 650 655  
 Asn Arg Glu Glu Lys Ile Glu Tyr Arg His Ser Asn Asn Gln His His  
 660 665 670  
 Ala Gly Tyr Tyr Thr Lys Asp Thr Leu Lys Ala Val Glu Glu Ile Ile  
 675 680 685  
 Gly Thr Ser His Asn Asp Ile Phe Lys Gly Ser Lys Phe Asn Asp Ala  
 690 695 700  
 Phe Asn Gly Gly Asp Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asn  
 705 710 715 720  
 Asp Arg Leu Phe Gly Gly Lys Gly Asp Asp Ile Leu Asp Gly Gly Asn  
 725 730 735  
 Gly Asp Asp Phe Ile Asp Gly Gly Lys Gly Asn Asp Leu Leu His Gly  
 740 745 750  
 Gly Lys Gly Asp Asp Ile Phe Val His Arg Lys Gly Asp Gly Asn Asp  
 755 760 765  
 Ile Ile Thr Asp Ser Asp Gly Asn Asp Lys Leu Ser Phe Ser Asp Ser  
 770 775 780  
 Asn Leu Lys Asp Leu Thr Phe Glu Lys Val Lys His Asn Leu Val Ile  
 785 790 795 800  
 Thr Asn Ser Lys Lys Glu Lys Val Thr Ile Gln Asn Trp Phe Arg Glu  
 805 810 815  
 Ala Asp Phe Ala Lys Glu Val Pro Asn Tyr Lys Ala Thr Lys Asp Glu  
 820 825 830  
 Lys Ile Glu Glu Ile Ile Gly Gln Asn Gly Glu Arg Ile Thr Ser Lys  
 835 840 845  
 Gln Val Asp Asp Leu Ile Ala Lys Gly Asn Gly Lys Ile Thr Gln Asp  
 850 855 860

Glu Leu Ser Lys Val Val Asp Asn Tyr Glu Leu Leu Lys His Ser Lys  
 865 870 875 880  
 Asn Val Thr Asn Ser Leu Asp Lys Leu Ile Ser Ser Val Ser Ala Phe  
 885 890 895  
 Thr Ser Ser Asn Asp Ser Arg Asn Val Leu Val Ala Pro Thr Ser Met  
 900 905 910  
 Leu Asp Gln Ser Leu Ser Ser Leu Gln Phe Ala Arg Gly Ser Cys Asn  
 915 920 925  
 Ile Val Pro Val Ser Ile Val Ser Arg Asn Ile Val Tyr Thr Arg Ala  
 930 935 940  
 Gln Pro Asn Gln Asp Ile Val  
 945 950

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "The amino acid at this location can be either Lys, Asp, Val or Asn."

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 5
  - (D) OTHER INFORMATION: /note= "The amino acid at this location can be either Lys, Asp, Val or Asn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Xaa Gly Xaa Asp  
 1 5